

10664423-3vsscn1a_rat.txt

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 5, 2008, 12:26:52 ; Search time 1 Seconds
(without alignments)
4.036 Million cell updates/sec

Title: us-10-664-423a-3
Perfect score: 10403
Sequence: 1 MEQTVLVPPGPDSNFFTRE. TKPI VEKHEQEKGDEKAKGK 2009

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1 seqs, 2009 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: scn1a_rat.uniprot_sprot:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match Length	DB ID	Description
1	10258	98.6	2009	1	SCN1A_RAT	Sodium channel protein

ALIGNMENTS

RESULT 1

SCN1A_RAT			
ID	SCN1A_RAT	STANDARD;	PRT; 2009 AA.
AC	P04774;		
DT	13-AUG-1987	integrated into UniProtKB/Swiss-Prot.	
DT	13-AUG-1987	sequence version 1.	
DT	27-JUN-2006	entry version 67.	
DE	Sodium channel protein type 1 subunit alpha (Sodium channel protein type 1 subunit alpha) (Voltage-gated sodium channel subunit alpha).		
DE	(Sodium channel protein, brain 1 subunit alpha).		
GN	Name=Scn1a;		
OS	Rattus norvegicus (Rat).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathii;		
CC	Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		

RP NUCLEOTI DE SEQUENCE [mRNA].
 RX MEDL1 NE=86146901; PubMed=3754035; DOI=10.1038/320188a0;
 RA Noda M, Ikeda T, Kayano T, Suzuki H, Takeshima H, Kurasaki M,
 RA Takahashi H, Numa S;
 RT "Existence of distinct sodium channel messenger RNAs in rat brain.";
 RL Nature 320: 188-192(1986).
 [2]
 RP NUCLEOTI DE SEQUENCE [mRNA].
 RX MEDL1 NE=87311395; PubMed=2442385;
 RA Noda M, Numa S;
 RT "Structure and function of sodium channel .";
 RL J. Recept. Res. 7: 467-497(1987).
 [3]
 RP NUCLEOTI DE SEQUENCE [mRNA] OF 177-253.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDL1 NE=92051314; PubMed=1658739;
 RA Sarao R, Gupta S. K, Auld V. J., Dunn R. J.;
 RT "Developmentally regulated alternative RNA splicing of rat brain sodium channel mRNAs.";
 RL Nucleic Acids Res. 19: 5673-5679(1991).
 CC -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium selective channel through which Na(+) ions may pass in accordance with their electrochemical gradient.
 CC -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-3 smaller ones. This sequence represents a large polypeptide.
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
 CC -!- DOMAIN: The sequence contains 4 internal repeats, each with 5 hydrophobic segments (S1, S2, S3, S5, S6) and one positively charged segment (S4). Segments S4 are probably the voltage-sensors and are characterized by a series of positively charged amino acids at every third position.
 CC -!- SIMILARITY: Belongs to the sodium channel family.
 CC -!- SIMILARITY: Contains 1 IQ domain.
 CC Copyrighted by the UniProt Consortium see <http://www.uniprot.org/terms>
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 DR EMBL; X03638; CAA27286.1; -; mRNA.
 DR EMBL; M22253; AAA79965.1; -; mRNA.
 DR PR; A25019; A25019.
 DR UniGene; RN:32079; -.
 DR HSSP; P04775; 1BYY.
 DR RGD; 69364; Scn1a.
 DR GO; GO:0005248; F: voltage-gated sodium channel activity; TAS.
 DR GO; GO:0019228; P: generation of action potential; TAS.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR011992; EF-Hand_type.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_CaM_bdg_region.
 DR InterPro; IPR005820; M-channel_nl_g.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR008051; Na_channel_1.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF000520; Ion_trans; 4.
 DR Pfam; PF00612; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR PRINTS; PR01664; NACHANNEL.
 DR PROSITE; PS50096; IQ; FALSE_NEG.
 KW Glycoprotein; Ion transport; Ion channel; Membrane; Repeat; Sodium

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KW Sodi um channel ; Sodi um t ransport ; Transmbrane; Transport ;
 KW Vol tage-gated channel .
 FT CHAIN 1 2009 Sodi um channel protein type 1 subunit
 alpha.
 FT /FTI=d-PRO_0000048490.
 FT TRANSMEM 124 147 S1 of repeat |.
 FT TRANSMEM 156 175 S2 of repeat |.
 FT TRANSMEM 189 207 S3 of repeat |.
 FT TRANSMEM 214 233 S4 of repeat |.
 FT TRANSMEM 250 273 S5 of repeat |.
 FT TRANSMEM 400 425 S6 of repeat |.
 FT TRANSMEM 763 787 S1 of repeat ||.
 FT TRANSMEM 799 822 S2 of repeat ||.
 FT TRANSMEM 831 850 S3 of repeat ||.
 FT TRANSMEM 857 876 S4 of repeat ||.
 FT TRANSMEM 893 913 S5 of repeat ||.
 FT TRANSMEM 967 992 S6 of repeat ||.
 FT TRANSMEM 1214 1237 S1 of repeat |||.
 FT TRANSMEM 1251 1276 S2 of repeat |||.
 FT TRANSMEM 1283 1304 S3 of repeat |||.
 FT TRANSMEM 1309 1330 S4 of repeat |||.
 FT TRANSMEM 1350 1377 S5 of repeat |||.
 FT TRANSMEM 1457 1483 S6 of repeat |||.
 FT TRANSMEM 1537 1560 S1 of repeat IV.
 FT TRANSMEM 1572 1595 S2 of repeat IV.
 FT TRANSMEM 1602 1625 S3 of repeat IV.
 FT TRANSMEM 1636 1657 S4 of repeat IV.
 FT TRANSMEM 1673 1695 S5 of repeat IV.
 FT TRANSMEM 1762 1786 S6 of repeat IV.
 FT REPEAT 110 454 |.
 FT REPEAT 750 1022 ||.
 FT REPEAT 1200 1514 |||.
 FT REPEAT 1523 1821 IV.
 FT CARBOHYD 211 211 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 284 284 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 295 295 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 301 301 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 306 306 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 338 338 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 601 601 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 621 621 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 681 681 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 892 892 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 1060 1060 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 1064 1064 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 1080 1080 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 1146 1146 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 1378 1378 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 1392 1392 N-linked (G cNAc. . .) (Potenti al).
 FT CARBOHYD 1403 1403 N-linked (G cNAc. . .) (Potenti al).
 SQ SEQUENCE 2009 AA; 228770 MV 6808466F6368373B CR064;

Query Match 98.6% Score 10258; DB 1; Length 2009;
 Best Local Similarity 98.2% Pred. No. 0;
 Matches 1972; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MEQTVLVPPGPDSFNFFTRESLAAIERR AEEKAKNPKPDKDDDENGPKPNSDLEAGKN 60
 Db 1 MEQTVLVPPGPDSFNFFTRESLAAIERR AEEKAKNPKPDKDDDENGPKPNSDLEAGKN 60
 Qy 61 LPFI YGDI PPEM/SEPLEDLPYII NKKTFI VLNGKAI FRFSATSALYI LTPFNPLRKI 120
 Db 61 LPFI YGDI PPEM/SEPLEDLPYII NKKTFI VLNGKAI FRFSATSALYI LTPFNPLRKI 120

Qy 121 AI KI LVHSLFSMLI MCTI LTNCFMMSNPPDWTKNVEYTFGTI YTFESLI KI I ARGFCL 180
 Db 121 AI KI LVHSLFSMLI MCTI LTNCFMMSNPPDWTKNVEYTFGTI YTFESLI KI I ARGFCL 180
 Qy 181 EDFTFLRDPWNLDFTVI TFAYVTEFVDLGNVSLRTFRLRALKTI SVI PGLKTI VGAL 240
 Db 181 EDFTFLRDPWNLDFTVI TFAYVTEFVDLGNVSLRTFRLRALKTI SVI PGLKTI VGAL 240
 Qy 241 | QSVKQLSDVM LTVFCLSVFALI GLQLFMCNLRNKCI QMPPTNASLEEHSI EKNI TVNY 300
 Db 241 | QSVKQLSDVM LTVFCLSVFALI GLQLFMCNLRNKCVQMPPTNASLEEHSI EKNTTDY 300
 Qy 301 NGTLI NETVFEFDWKSYI QDSRYHYFLEGFLDALLCGNSSDAGQCOPEGYMCVKAGRPNY 360
 Db 301 NGTLVNETVFEFDWKSYI QDSRYHYFLEGFLDALLCGNSSDAGQCOPEGYMCVKAGRPNY 360
 Qy 361 GYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYM FFVLVI FLGSFYLI NLI LA 420
 Db 361 GYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYM FFVLVI FLGSFYLI NLI LA 420
 Qy 421 VVAMAYEECNQATLEEAECQEAEFQOM EQLKKQCEAAQQAATASEHSREPSAAGRLS 480
 Db 421 VVAMAYEECNQATLEEAECQEAEFQOM EQLKKQCEAAQQAATASEHSREPSAAGRLS 480
 Qy 481 DSSSEASKLSSSAKEERRNRRKKRKQCEOSGEEKDEDEFQKSESEDSDI RRKGFRFSI EG 540
 Db 481 DSSSEASKLSSSAKEERRNRRKKRKQCEQSGEEKDDDEFHKSESEDSDI RRKGFRFSI EG 540
 Qy 541 NRLTYEKRYSSPHQSLLSI RGSLFSPPRNSRTSLSFSFRGRAKDVGSENDFADDEHSTFED 600
 Db 541 NRLTYEKRYSSPHQSLLSI RGSLFSPPRNSRTSLSFSFRGRAKDVGSENDFADDEHSTFED 600
 Qy 601 NESRRDSLFPVPRRHGERRNSNL SQTSRSSPM AVFPANGKMSTVDONG/VSLVGGPSVP 660
 Db 601 NESRRDSLFPVPRRHGERRNSNL SQTSRSSPM AGLPANGKMSTVDONG/VSLVGGPSVP 660
 Qy 661 TSPVGQLLPEVI | DKPATDDNGTTTEEMRKPRSSSFHVSMDFLEDPSQRQRAMS| ASI L 720
 Db 661 TSPVGQLLPEVI | DKPATDDNGTTTEEMRKPRSSSFHVSMDFLEDPSQRQRAMS| ASI L 720
 Qy 721 TNTVEELEESRQKCPPWYKFSNI FLI WDCSPYWLKVKHVNLLVMDPFVLDLAI TI CI VL 780
 Db 721 TNTVEELEESRQKCPPWYKFSNI FLI WDCSPYWLKVKH VNLLVMDPFVLDLAI TI CI VL 780
 Qy 781 NTLFNAMEIHYPMIDHFNNVLTVGNLVTFTI FTAEMFLKI I ANDPYYYFCEGWN| FDGF| V 840
 Db 781 NTLFNAMEIHYPMIEHFNHVLTVGNLVTFTI FTAEMFLKI I ANDPYYYFCEGWN| FDGF| V 840
 Qy 841 TLSLVELGLANVEGLSVLRSFRLRVFKLAKSWPTLNMLI KI I GNSVGALGNLTIVLAI | 900
 Db 841 TLSLVELGLANVEGLSVLRSFRLRVFKLAKSWPTLNMLI KI I GNSVGALGNLTIVLAI | 900
 Qy 901 VFI FAVVGVLQFGKSYKDCVOKI ASDCOLPRWHMDFFHSFLI VFRVLCGEW ETMDCM 960
 Db 901 VFI FAVVGVLQFGKSYKDCVOKI ATDCKLPRWHMDFFHSFLI VFRVLCGEW ETMDCM 960
 Qy 961 EVAGQAMCLTVFMMWI GNLVLLNLFLALLLSSFSADNLAA TDDNEMNLIQI AVDRM 1020
 Db 961 EVAGQAMCLTVFMMWI PNLVLLNLFLALLLSSFSADNLAA TDDNEMNLIQI AVDRM 1020
 Qy 1021 KGVA/YVKRKI YEFI QOSFI RKGKI LDEI KPLDDLNNKKDSCVSNHTAEI GKLDLGYLKDVN 1080

Db 1021 KGIVAYVKRKI YEFI QGSFVVKQKQI LDEI KPLDOLNNRKDNCTSNTTEI GKDLDCLKDVN 1080
 Qy 1081 GTTSGI GTGSSEVKEYI I DESDYMFSI NNPSLTVTVPI AVGESDFENLNTEDFSSESDEE 1140
 Db 1081 GTTSGI GTGSSEVKEYI I DESDYMFSI NNPSLTVTVPI AVGESDFENLNTEDFSSESDEE 1140
 Qy 1141 SKEKLNESSSSSEGSTVDI GAPVEEOPWEEPEETLEPEACFTEGCVQRFKOCQI NVEEGR 1200
 Db 1141 SKEKLNESSSSSEGSTVDI GAPAEEOVMEPEETLEPEACFTEGCVQRFKOCQI SVEEGR 1200
 Qy 1201 GKQWNLRRTCFRI VEHNWFETFI VFM LLSSGALAFEDI YI DQRKTI KTMLEYADKVFT 1260
 Db 1201 GKQWNLRRTCFRI VEHNWFETFI VFM LLSSGALAFEDI YI DQRKTI KTMLEYADKVFT 1260
 Qy 1261 YI FI LEMLKWWAYGYQTYFTNAWCDFLI VDVSLSVSLTANALGYSELGAI KSLRTLRA 1320
 Db 1261 YI FI LEMLKWWAYGYQTYFTNAWCDFLI VDVSLSVSLTANALGYSELGAI KSLRTLRA 1320
 Qy 1321 LRPLRALSRFEGMRVWNALLGAI PSI MNVLLVCL1 FWL1 FSI MGVLNFAGKFYHICNTT 1380
 Db 1321 LRPLRALSRFEGMRVWNALLGAI PSI MNVLLVCL1 FWL1 FSI MGVLNFAGKFYHCVNTT 1380
 Qy 1381 TGDRFDI EDVNNTDCLKLI ERNETARMVKVNFDNVFGYLSSLQVATFKGMDI MYA 1440
 Db 1381 TGDFEI TEVNNHSDCDLKLI ERNETARMVKVNFDNVFGYLSSLQVATFKGMDI MYA 1440
 Qy 1441 AVDSRNVELCPKYEESLYMLYFV1 FI I FGFSFTLNLFI GVI I DNFNQKKKFGQDI FM 1500
 Db 1441 AVDSRNVELCPKYEESLYMLYFV1 FI I FGFSFTLNLFI GVI I DNFNQKKKFGQDI FM 1500
 Qy 1501 TEEQKYYNAMKKLGSKKPKQPKI PRPGNKFQGM/FDFVTRQVFDI SI M LI CLNM/TMM 1560
 Db 1501 TEEQKYYNAMKKLGSKKPKQPKI PRPGNKFQGM/FDFVTRQVFDI SI M LI CLNM/TMM 1560
 Qy 1561 ETDDOSEYVTI LSRI NLVFI VLFTGECVLKL1 SLRHYYFTI GWNI FDFVWVI LSI VGMF 1620
 Db 1561 ETDDOSDYVTI LSRI NLVFI VLFTGECVLKL1 SLRHYYFTI GWNI FDFVWVI LSI VGMF 1620
 Qy 1621 LAELI EKYFVSPTLFRV1 RLARI GRI LRL1 KGAKG1 RTLLFALMMSLPALFNI GLLLFLV 1680
 Db 1621 LAELI EKYFVSPTLFRV1 RLARI GRI LRL1 KGAKG1 RTLLFALMMSLPALFNI GLLLFLV 1680
 Qy 1681 MFI YAI FGIVSNFAYVKREVG1 DDMNFETFGNSM CLFQI TTSAQWDGLAPI LNSKPPD 1740
 Db 1681 MFI YAI FGIVSNFAYVKREVG1 DDMNFETFGNSM CLFQI TTSAQWDGLAPI LNSKPPD 1740
 Qy 1741 CDPNKNPGSSVKGDCDNPSVG1 FFFFVSYI I SFLVVVNMY1 AVI LENFSVATEESAEP1 1800
 Db 1741 CDPNKNPGSSVKGDCDNPSVG1 FFFFVSYI I SFLVVVNMY1 AVI LENFSVATEESAEP1 1800
 Qy 1801 SEDDFEMFYEWKEFKDPDATCFMEFEKLQSOAAALEPPLNLPCPNKLQLI AMDLPM/SGD 1860
 Db 1801 SEDDFEMFYEWKEFKDPDATCFMEFEKLQSOAAALEPPLNLPCPNKLQLI AMDLPM/SGD 1860
 Qy 1861 RI HCLDI LFATFKRVLGESGEMDALRI QMEERFMASNPSKVSYQPI TTTLKRKQEEVSAV 1920
 Db 1861 RI HCLDI LFATFKRVLGESGEMDALRI QMEERFMASNPSKVSYQPI TTTLKRKQEEVSAV 1920
 Qy 1921 I CRAYRRHLLKRTVKQASFTYNNKNI KGGANLLI KEDM I DRI NENSI TEKTDLMSTA 1980
 Db 1921 I CRAYRRHLLKRTVKQASFTYNNKNI KGGANLLVKEDM I DRI NENSI TEKTDLMSTA 1980
 Qy 1981 ACPPSYDRVTKPI VEKHEQEGKDEAKGK 2009

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Db 1981 ACPPSYDRVTKPI VEKHECEGKDEKAKGK 2009

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